

REMARKS

Claims 1-13 are pending. No amendments have been made by way of the present submission, thus, no new matter has been added.

In the outstanding Office the Examiner has required Applicants to elect one of the following two groups. In particular, the Examiner has asserted that these groups are not so linked so as to form a single general inventive concept under PCT Rule 13.1;

Group I, claims 1-8, drawn to a transposon nucleic acid sequence.

Group II, claims 9-13, drawn to a method of producing a deletion derivative of a polypeptide coding sequence.

Applicants respectfully disagree with the Examiner. The Examiner has asserted that the inventions listed in Groups I and II fail to form a single general inventive concept under PCT Rule 13.1 because, pursuant to PCT Rule 13.2, they lack the same or corresponding special technical feature. For instance, even though both of these groups involve a transposon nucleic acid comprising a genetically engineered translation stop signal in three reading frames at least partly within a transposon end sequence recognized by a transposase, the Examiner asserts that this does not represent a contribution over the prior art. Applicants respectfully disagree with the Examiner.

The Examiner has alleged that features recited in claim 1 have been disclosed in prior art, for example in Coros et al. (2001). This is incorrect. The present invention discloses methods and materials for producing C-terminal deletion derivatives of polypeptide encoding nucleic acids by the use of a modified transposon with stop codons in all three reading frames, said stop codons residing at least partly within the transposon end sequence recognized and bound by a

transposase, which catalyse the transposition.

The problem to be solved by the invention is to generate a number of deletion derivatives simultaneously and with ease. The solution of the invention is achieved by placing stop codons at least partly within the transposon end, which strategy leaves at its best no extra amino acid residues in the C-terminus of a deletion derivative obtained by the present method.

Coros et al. disclose the modification of the conserved CA dinucleotide and the nearest flanking nucleotides thereof at Mu termini (see Fig. 2 of Coros et al.). The same conserved CA dinucleotide can be seen at the utmost left end of the lower strand of Cat-Mu transposon in Fig. 2 of the present specification, where the previously known transposons Cat-Mu and Cat-Mu(NotI) are compared to the Cat-Mu(Stop x 3) transposon of the present invention.

Coros et al. shows only single mutations which were made one at the time to different positions of the Mu end at or near the CA nucleotide. Thus, Coros et al. is not a bar to the present invention, since the possibility to introduce a functional sequence, such as stop codons, in the Mu end is not disclosed. Moreover, the conserved CA dinucleotide and the nearest flanking nucleotides thereof do not reside in Mu transposon end sequences called R1 or R2. This makes evident that the packed nature of the Mu end hinders the engineering of three stop codons (i.e. TGA, TAG and/or TAA) to the position, if modifications to the R1 or R2 region are not made. Since no mutations in R1, R2 or corresponding L1 sequences are shown, Coros et al. cannot either anticipate or render obvious the present invention.

For instance, in one of the preferred embodiments of the invention, i.e. transposon Cat-Mu(Stop x 3), the distal terminus and R1 region of the Mu transposon end are mutated so that three TGA codons in three reading frames are formed (refer to nucleotides 5, 6, 7; 9, 10, 11; and

13, 14, 15 counted from the left end of the upper strand of Cat-Mu(Stop x 3) shown in Fig. 2 of the present specification; the mutated nucleotides are marked with an asterisk).

In summary, Coros et al. fails to suggest or disclose the features of claims 1 and 9 due to the following:

- 1) Coros et al. do not disclose stop codons in three reading frames at least partly within a transposon end;
- 2) only single point mutations to a Mu end are shown, although it is clear that a number of (possibly adjacent) point mutations is needed to create functional stop codons in three reading frames; and
- 3) no mutations to Mu R1 or R2 sequence are shown.

Therefore, the present invention represents a contribution over the prior art.

In view of the above, Applicants respectfully submit that the present claims, for instance of Group I and Group II, do relate to a single general inventive concept sharing the same technical feature. Thus, the Examiner's Unity of the Invention rejection is improper. In fact, all presently pending claims share unity of invention.

However, in order to be fully responsive to the outstanding Office Action, Applicants hereby elect the claims of Group I. This is an election with traverse.

Further, Applicants draw the Examiner's attention to the fact that the claims of Group II represent methods of using the product of claim 1 (Group I), thus, once allowable subject matter is indicated for the product of claim 1, any method of use claims, for instance of Group II, which include all allowable limitations of the product claim, should be rejoined.

The Examiner has further indicated that Group I is further restricted to a single sequence

for examination. Applicants respectfully disagree with the Examiner's assertion that in most cases only one independent and distinct sequence will be examined in a single application without restriction. In this regard, Applicants refer the Examiner to the Commissioner's *sua sponte* decision to partially waive 37 C.F.R. § 1.475 and 1.499 *et seq.* to permit Applicants to claim up to ten (10) nucleotide sequences that do not have the same or corresponding special technical feature. Refer to MPEP § 1850 under the heading "Unity of Invention – Nucleotide Sequences" (see MPEP page 1800-103, May 2004 Edition).

However, in order to be fully responsive, Applicants hereby elect SEQ ID NO:1. This is an election with traverse.

Favorable action on the merits is respectfully solicited.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. § 1.16 or under 37 C.F.R. § 1.17; particularly, extension of time fees.

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Respectfully submitted,

  
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